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FEB 19 2003

TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING

DATE: 02/12/2003

PATENT APPLICATION: US/09/578,900A

TIME: 10:44:02

Input Set : A:\032796-019.ST25.txt

Output Set: N:\CRF4\02112003\I578900A.raw

4 <110> APPLICANT: Carulli, John P.
5 Little, Randall D.
6 Recker, Robert R.
7 Johnson, Mark L.

9 <120> TITLE OF INVENTION: REGULATING LIPID LEVELS VIA THE ZMAX1 OR HBM GENE

11 <130> FILE REFERENCE: 032796-019

13 <140> CURRENT APPLICATION NUMBER: US 09/578,900A

14 <141> CURRENT FILING DATE: 2000-05-26

16 <150> PRIOR APPLICATION NUMBER: US 09/543,771

17 <151> PRIOR FILING DATE: 2000-04-05

19 <150> PRIOR APPLICATION NUMBER: US 09/229,319

20 <151> PRIOR FILING DATE: 1999-01-13

22 <150> PRIOR APPLICATION NUMBER: US 60/071,449

23 <151> PRIOR FILING DATE: 1998-01-13

25 <150> PRIOR APPLICATION NUMBER: US 60/105,511

26 <151> PRIOR FILING DATE: 1998-10-23

28 <160> NUMBER OF SEQ ID NOS: 73

30 <210> SEQ ID NO: 1

31 <211> LENGTH: 5120

32 <212> TYPE: DNA

33 <213> ORGANISM: Homo sapiens

35 <400> SEQUENCE: 1

37 actaaagcgc cgccgccgcg ccatggagcc cgagtgcgcg cggcgcgggc ccgtccggcc 60
38 gccggacaac atg gag gca gcg ccg ccc ggg ccg ccg tgg ccg ctg ctg 109
39 Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
40 1 5 10

41 ctg ctg ctg ctg ctg ctg ctg gcg ctg tgc ggc tgc ccg gcc ccc gcc 157
42 Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
43 15 20 25

44 gcg gcc tcg ccg ctc ctg cta ttt gcc aac cgc cgg gac gta cgg ctg 205
45 Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
46 30 35 40 45

47 gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc 253
48 Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
49 50 55 60

50 ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg 301
51 Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
52 65 70 75

53 tac tgg aca gac gtg agc gag gag gcc atc aag cag acc tac ctg aac 349
54 Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn
55 80 85 90

56 cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc ggc ctg gtc tct 397
57 Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser

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58	95	100	105		445
59	ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg				
60	Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr				
61	110	115	120		493
62	gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc				
63	Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser				
64	130	135			541
65	cgg aag gtg ctc ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc				
66	Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala				
67	145	150	155		589
68	ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg ggt gag acg				
69	Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr				
70	160	165	170		637
71	ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att				
72	Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile				
73	175	180	185		685
74	gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag				
75	Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu				
76	190	195	200		733
77	gag cag aag ctc tac tgg gct gac gcc aag ctc agc ttc atc cac cgt				
78	Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg				
79	210	215	220		781
80	gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg				
81	Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu				
82	225	230	235		829
83	acg cac ccc ttc gcc ctg acg ctc tcc ggg gac act ctg tac tgg aca				
84	Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr				
85	240	245	250		877
86	gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg				
87	Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly				
88	255	260	265		925
89	aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag				
90	Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln				
91	270	275	280		973
92	gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag				
93	Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu				
94	290	295	300		1021
95	gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct				
96	Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro				
97	305	310	315		1069
98	ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac gcc				
99	Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly				
100	320	325	330		1117
101	agg acg tgt aag gca gga gcc gag gtg ctg ctg ctg gcc cgg cgg				
102	Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg				
103	335	340	345		1165
104	acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gac atc				
105	Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile				
106	350	355	360		365

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107	gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac	1213
108	Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp	
109	370 375 380	
110	ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc	1261
111	Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile	
112	385 390 395	
113	cgc agg gcg tac ctg gac ggg tct ggg gcg cag acg ctg gtc aac acc	1309
114	Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr	
115	400 405 410	
116	gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac	1357
117	Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn	
118	415 420 425	
119	ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc	1405
120	Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu	
121	430 435 440 445	
122	aac ggc acc tcc cgc aag atc ctg gtg tgc gag gac ctg gac gag ccc	1453
123	Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro	
124	450 455 460	
125	cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac	1501
126	Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp	
127	465 470 475	
128	tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag	1549
129	Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu	
130	480 485 490	
131	cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc	1597
132	Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala	
133	495 500 505	
134	ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac	1645
135	Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp	
136	510 515 520 525	
137	aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg	1693
138	Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu	
139	530 535 540	
140	gag gac aag ctc cgc cac att ttc ggg ttc acg ctg ctg ggg gac ttc	1741
141	Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe	
142	545 550 555	
143	atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag	1789
144	Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys	
145	560 565 570	
146	gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg	1837
147	Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met	
148	575 580 585	
149	ggg ctc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac cgg tgt	1885
150	Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys	
151	590 595 600 605	
152	gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac	1933
153	Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His	
154	610 615 620	
155	gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg	1981

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156	Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met	
157	625 630 635	2029
158	aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc	
159	Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala	
160	640 645 650	2077
161	gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc	
162	Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asp Val Ala Ile	
163	655 660 665	2125
164	ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc	
165	Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser	
166	670 675 680 685	2173
167	aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc	
168	Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg	
169	690 695 700	2221
170	gcc ttc atg aac ggg agc tgg gtg gag cac gtg gtg gag ttt ggc ctt	
171	Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu	
172	705 710 715	2269
173	gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac	
174	Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr	
175	720 725 730	2317
176	tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg	
177	Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly	
178	735 740 745	2365
179	cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tgc	
180	Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser	
181	750 755 760 765	2413
182	ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc	
183	Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly	
184	770 775 780	2461
185	ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg	
186	Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met	
187	785 790 795	2509
188	acg ctg gtg gac aag gtg ggc cgg gcc aac gac ctc acc att gac tac	
189	Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr	
190	800 805 810	2557
191	gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag	
192	Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu	
193	815 820 825	2605
194	tcg tcc aac atg ctg ggt cag gag cgg gtc gtg att gcc gac gat ctc	
195	Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu	
196	830 835 840 845	2653
197	ccg cac ccg ttc ggt ctg acg cag tac agc gat tat atc tac tgg aca	
198	Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr	
199	850 855 860	2701
200	gac tgg aat ctg cac agc att gag cgg gcc gac aag act agc ggc cgg	
201	Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg	
202	865 870 875	2749
203	aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg	
204	Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu	

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205	880	885	890	2797
206	gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tgt atg cac aac			
207	Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn			
208	895	900	905	2845
209	aac ggg cag tgt ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc			
210	Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg			
211	910	915	920	2893
212	tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc			
213	Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys			
214	930	935	940	2941
215	agc ccg ccc acc acc ttc ttg ctg ttc agc cag aaa tct gcc atc agt			
216	Ser Pro Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser			
217	945	950	955	2989
218	cgg atg atc ccg gac gac cag cac agc ccg gat ctc atc ctg ccc ctg			
219	Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu			
220	960	965	970	3037
221	cat gga ctg agg aac gtc aaa gcc atc gac tat gac cca ctg gac aag			
222	His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys			
223	975	980	985	3085
224	ttc atc tac tgg gtg gat ggg cgc cag aac atc aag cga gcc aag gac			
225	Phe Ile Tyr Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp			
226	990	995	1000	3133
227	gac ggg acc cag ccc ttt gtt ttg acc tct ctg agc caa ggc caa aac			
228	Asp Gly Thr Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn			
229	1010	1015	1020	3181
230	cca gac agg cag ccc cac gac ctc agc atc gac atc tac agc cgg aca			
231	Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr			
232	1025	1030	1035	3229
233	ctg ttc tgg acg tgc gag gcc acc aat acc atc aac gtc cac agg ctg			
234	Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu			
235	1040	1045	1050	3277
236	agc ggg gaa gcc atg ggg gtg gtg ctg cgt ggg gac cgc gac aag ccc			
237	Ser Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro			
238	1055	1060	1065	3325
239	agg gcc atc gtc gtc aac gcg gag cga ggg tac ctg tac ttc acc aac			
240	Arg Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn			
241	1070	1075	1080	3373
242	atg cag gac cgg gca gcc aag atc gaa cgc gca gcc ctg gac ggc acc			
243	Met Gln Asp Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr			
244	1090	1095	1100	3421
245	gag cgc gag gtc ctc ttc acc acc ggc ctc atc cgc cct gtg gcc ctg			
246	Glu Arg Glu Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu			
247	1105	1110	1115	3469
248	gtg gtg gac aac aca ctg ggc aag ctg ttc tgg gtg gac ggc gac ctg			
249	Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu			
250	1120	1125	1130	3517
251	aag cgc att gag agc tgt gac ctg tca ggg gcc aac cgc ctg acc ctg			
252	Lys Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu			
253	1135	1140	1145	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 12044,12489,26433,26434,26435,26436,26439,26441
Seq#:7; N Pos. 4336,4345,4349,4392,4447,4490
Seq#:8; N Pos. 33739,33749,33758
Seq#:9; N Pos. 8356,8385,38585